SFIG 1. The relative levels of hepatic mRNA for genes involved in transcriptional regulation, lipid metabolism, and glucose metabolism in *Pemt*$^{-/-}$ mice fed a chow diet. RNA was isolated from livers of fasting mice (4/group) and mRNA levels were determined by RT-qPCR. Data are presented relative to mRNA of cyclophilin in the same sample (* t test, $p < 0.05$). The abbreviations for the mRNAs are: PPAR, peroxisome proliferator activated receptor; SREBP, sterol response element-binding protein; LXR, liver X receptor; PGC, PPARγ co-activator; PEPCK, phosphoenolpyruvate carboxy kinase; G6Pase, glucose-6-P phosphatase; GK, glucose kinase; MCAD, medium chain acyl-CoA dehydrogenase; LCAD, long chain acyl-CoA dehydrogenase; CPT, carnitine:palmitoyl-CoA transferase; UCP, uncoupling protein; ACC, acetyl-CoA carboxylase; MCD, malonyl-CoA decarboxylase; SCD, stearoyl-CoA desaturase; FAS, fatty acid synthase; DGAT, diacylglycerol:acyl-CoA acyltransferase; TGH, triacylglycerol hydrolase; ATGL, adipose triacylglycerol lipase; HSL, hormone sensitive lipase.

SFIG 2: Macrophage infiltration in WAT taken from *Pemt*$^{+/+}$ mice fed a HF diet (A) WAT taken from *Pemt*$^{+/+}$ mice was fixed in 10% buffered-formalin and was stained with hematoxylin and eosin. Dark areas indicate the presence of macrophages within the sample. Each picture is a representative picture taken from different mice. (B) The size of individual adipocytes (n = 210-230 cells) was quantified using ImageJ software and is displayed using a box and whiskers plot (*, $P < 0.001$). (C and D) Adipocyte gene expression: RT-qPCR was performed on a Rotor-gene 3000 instrument using gene-specfic primers. RNA was isolated from WAT taken from 4-5 mice per group. Data are presented relative to mRNA of cyclophilin in the same sample and are expressed as mean ± SEM (*, $P < 0.05$). The abbreviations for the mRNAs are given in SFIG 1.

SFIG 3: Real-time quantitative PCR of hepatic lipid genes in mice fed a HF diet. Hepatic gene expression: mRNA levels for genes involved in transcriptional regulation, lipid metabolism, and glucose metabolism were determined by RT-qPCR. RNA was isolated from livers taken from fasting mice (3-4 per group). Data are presented relative to mRNA of cyclophilin in the same sample and are expressed as mean ± SEM (*, $P < 0.05$).

SFIG 4: HF-diet fed *Pemt*$^{-/-}$ mice have higher oxygen consumption than *Pemt*$^{+/+}$ mice. All results are presented as means ± SEM. Indirect calorimetry was performed using an Oxymax Lab Animal Monitoring System. Lean body mass was measured by nuclear magnetic resonance using the $LF90_{II}$ body composition analyzer (n=4/group). The ratio of lean body mass to total body mass was used to recalculate oxygen consumption data.

SFIG 5: Real-time quantitative PCR of hepatic lipid genes in mice fed a HFCS diet. Hepatic gene expression: mRNA levels for genes involved in transcriptional regulation, lipid metabolism, and glucose metabolism were determined by RT-qPCR. RNA was isolated from livers taken from fasting mice (4-5 per group). Data are presented relative to mRNA of cyclophilin in the same sample and are expressed as mean ± SEM (*, $P < 0.01$).

PC Species*	*Pemt*$^{+/+}$	*Pemt*$^{-/-}$	Relative Change
Total	16.0 ± 0.70	7.88 ± 0.69	↓
30:0	0.01 ± 0	0.02 ± 0	↑
32:2	0.01 ± 0	0.01 ± 0	=
32:1	0.07 ± 0.01	0.08 ± 0.01	=
32:0	0.20 ± 0.02	0.36 ± 0.02	↑
34:4	0.01 ± 0	0.01 ± 0	=
34:3	0.12 ± 0.01	0.07 ± 0.01	↓
34:2	1.91 ± 0.13	0.98 ± 0.13	↓
34:1	1.15 ± 0.05	0.90 ± 0.05	↓
34:0	0.04 ± 0.01	0.05 ± 0.01	↑
36:6	0.01 ± 0	0.01 ± 0	=
36:5	0.09 ± 0.005	0.04 ± 0	↓
36:4	3.33 ± 0.19	1.73 ± 0.19	↓
36:3	0.60 ± 0.03	0.34 ± 0.03	↓
36:2	1.09 ± 0.05	0.66 ± 0.05	↓
36:1	0.15 ± 0.01	0.15 ± 0.01	=
36:0	0.03 ± 0	0.03 ± 0	=
38:6	2.99 ± 0.22	0.61 ± 0.22	↓
38:5	0.59 ± 0.02	0.25 ± 0.02	↓
38:4	2.38 ± 0.09	1.21 ± 0.09	↓
38:3	0.23 ± 0.03	0.15 ± 0.02	=
38:2	0.02 ± 0	0.02 ± 0	=
40:6	0.95 ± 0.06	0.21 ± 0.06	↓

Supplementary Table 1: Hepatic PC species in *Pemt*$^{+/+}$ and *Pemt*$^{-/-}$ mice fed the HF diet
8-week-old male *Pemt*$^{+/+}$ and *Pemt*$^{-/-}$ mice were fed the HF diet for 10 weeks. PC values are expressed as nmol/mg liver tissue. Values are mean ± SEM. Arrows indicate significant difference (P<0.05) compared to *Pemt*$^{+/+}$ mice (n=5). * The number before the colon indicates number of carbons; the number after the colon indicates number of double bonds.

Figure S1

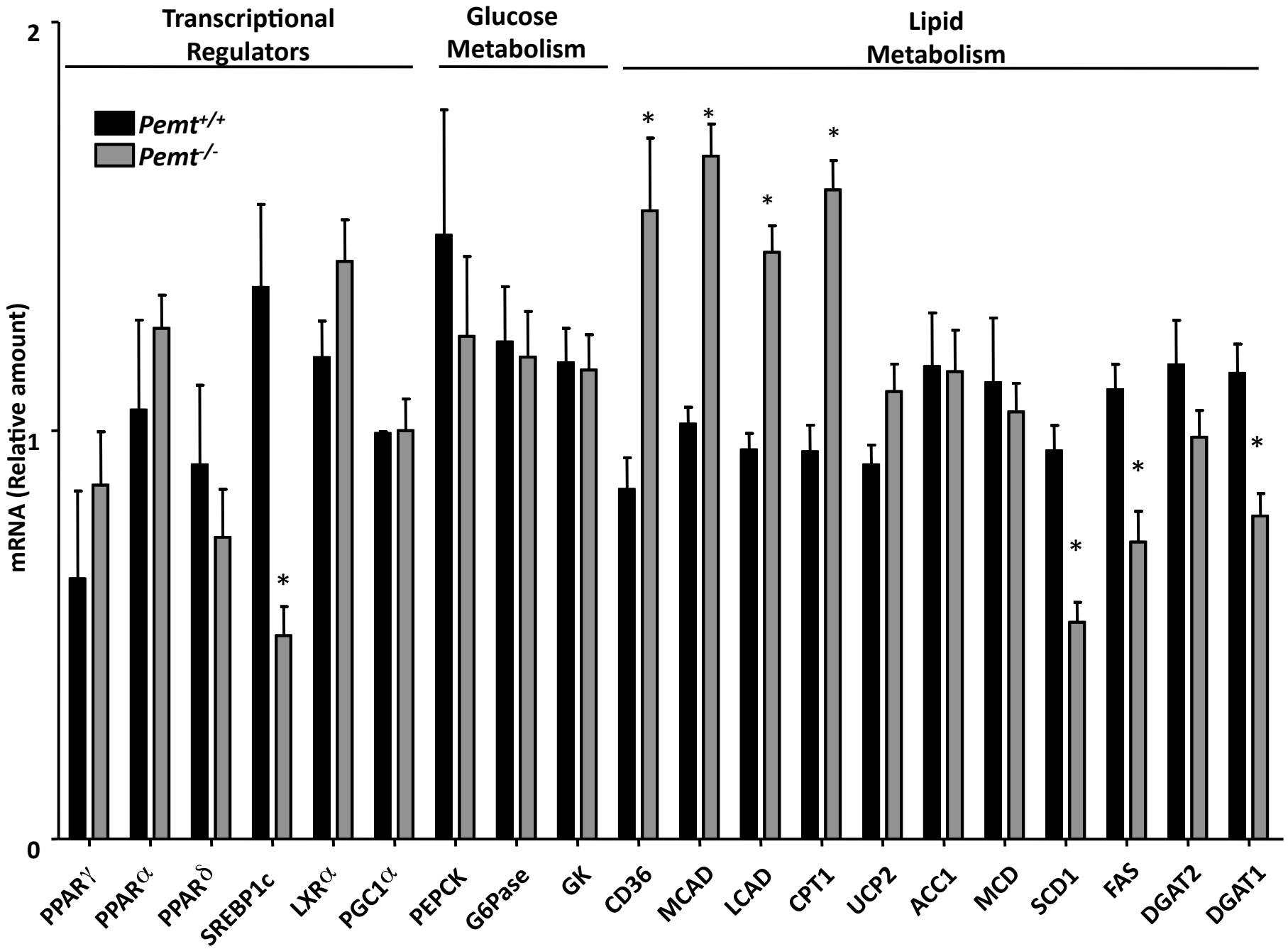

Transcriptional Regulators
Glucose Metabolism
Lipid Metabolism
Pemt+/+
Pemt-/-
mRNA (Relative amount)
2
1
0
*
PPARγ
PPARα
PPARδ
SREBP1c
LXRα
PGC1α
PEPCK
G6Pase
GK
CD36
MCAD
LCAD
CPT1
UCP2
ACC1
MCD
SCD1
FAS
DGAT2
DGAT1

Figure S2

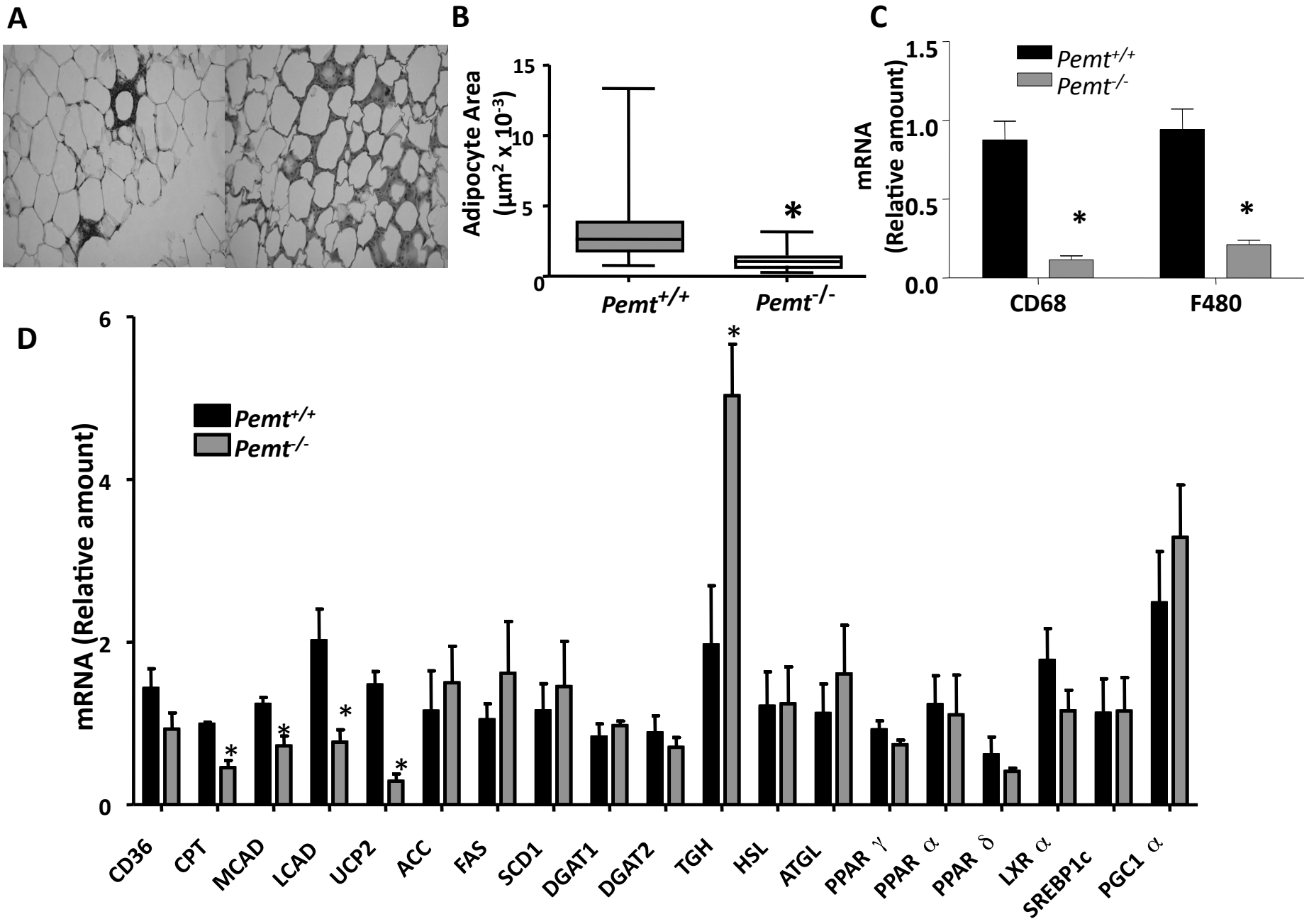

A
B
C
D
Adipocyte Area (μm² x 10⁻³)
15
10
5
0
Pemt+/+
Pemt-/-
*
mRNA (Relative amount)
1.5
1.0
0.5
0.0
CD68
F480
6
4
2
0
CD36
CPT
MCAD
LCAD
UCP2
ACC
FAS
SCD1
DGAT1
DGAT2
TGH
HSL
ATGL
PPAR γ
PPAR α
PPAR δ
LXR α
SREBP1c
PGC1 α

Figure S3

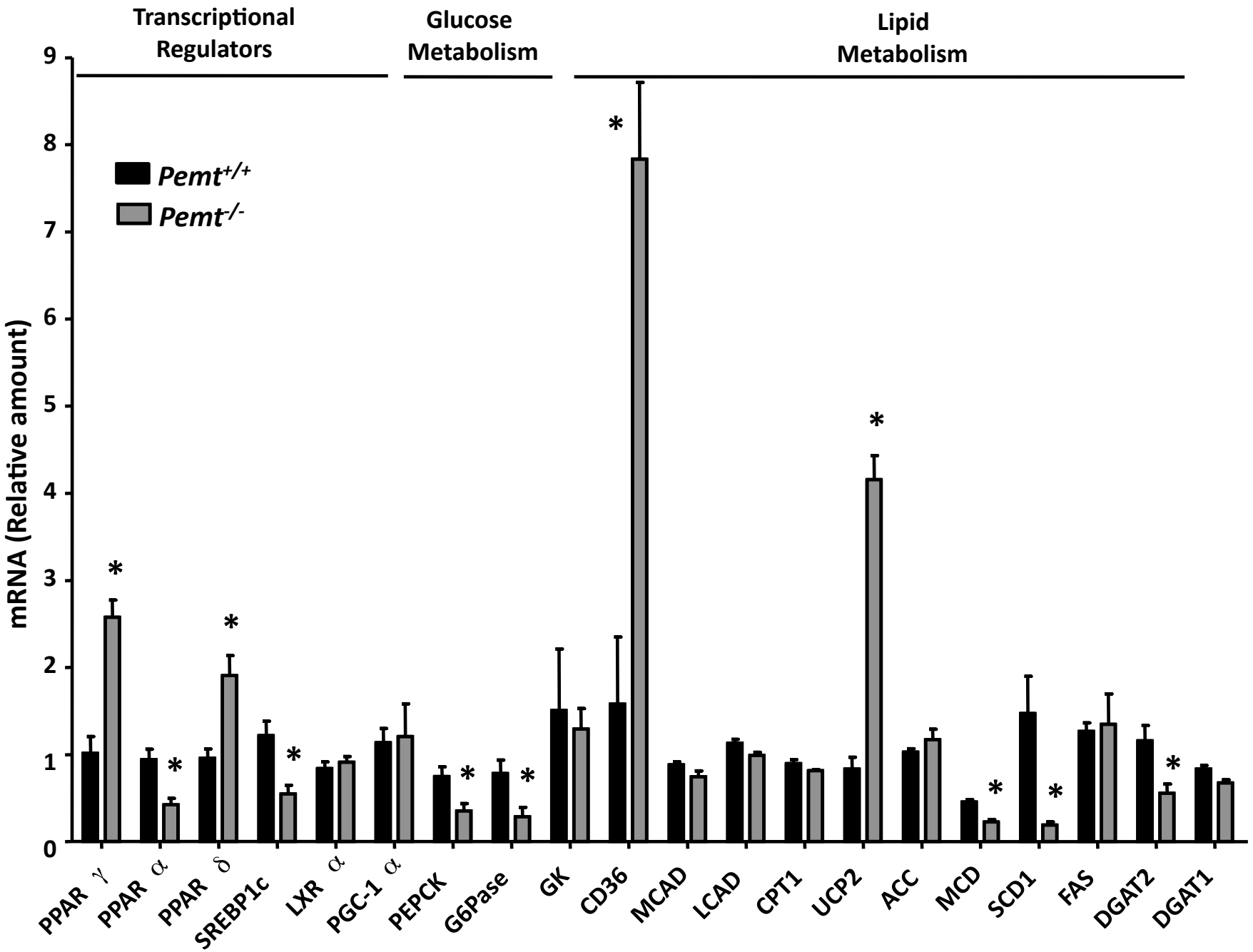

Transcriptional Regulators
Glucose Metabolism
Lipid Metabolism
Pemt+/+
Pemt-/-
mRNA (Relative amount)
0
1
2
3
4
5
6
7
8
9
PPAR γ
PPAR α
PPAR δ
SREBP1c
LXR α
PGC-1 α
PEPCK
G6Pase
GK
CD36
MCAD
LCAD
CPT1
UCP2
ACC
MCD
SCD1
FAS
DGAT2
DGAT1

Figure S4

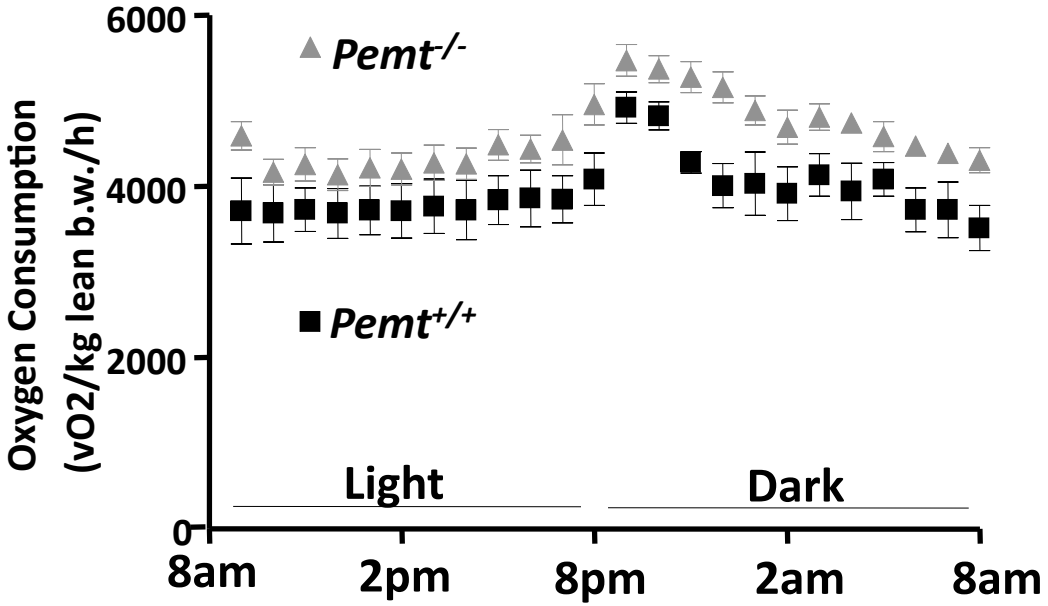
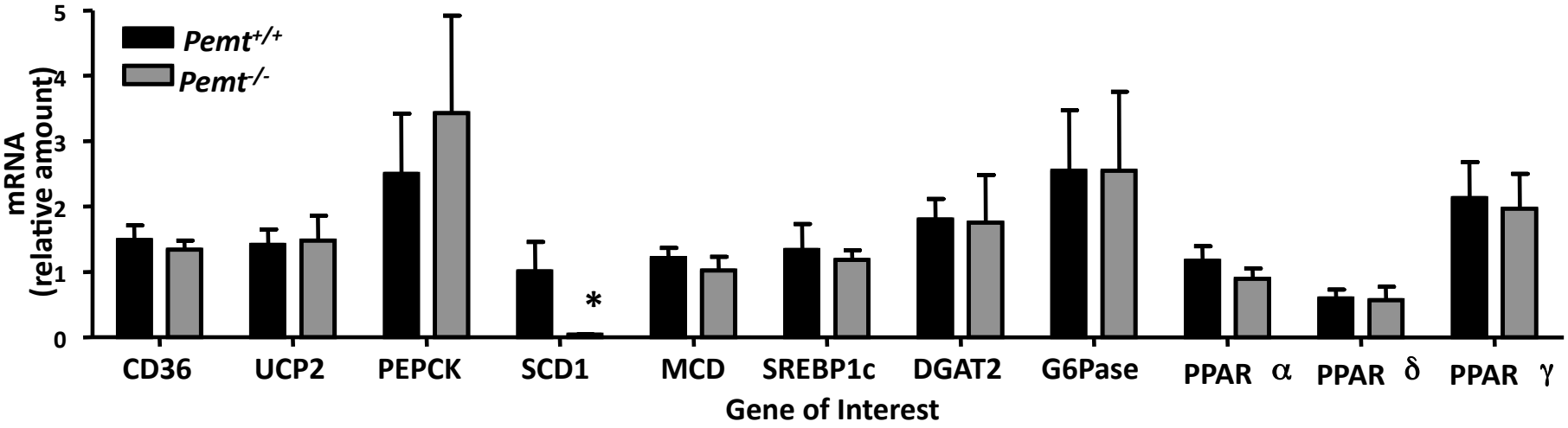

6000
4000
2000
0
Oxygen Consumption
(vO2/kg lean b.w./h)
Pemt-/-
Pemt+/+
Light
Dark
8am
2pm
8pm
2am
8am

Figure S5


Pemt+/+
Pemt-/-
mRNA (relative amount)
0
1
2
3
4
5
*
CD36
UCP2
PEPCK
SCD1
MCD
SREBP1c
DGAT2
G6Pase
PPAR α
PPAR δ
PPAR γ
Gene of Interest